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FIG. 1A

QUERY: 1 MAAGSRTSLLAFALLCLPWLQEAGAVQTVPLSRLEFDHAMLQAHRAHQLAIDTYQEFVSS 60
MAAGSRTSLLAFALLCLPWLQEAGAVQTVPLSRLEFDHAMLQAHRAHQLAIDTYQEF +
SBJCT: 1 MAAGSRTSLLAFALLCLPWLQEAGAVQTVPLSRLEFDHAMLQAHRAHQLAIDTYQEFEEET 60

QUERY: 61 W-----GMSIPTPSNMEETQOKSNLELLRISLLIESWLEPVRFLR 102
+ DSIPTPSNMEETQOKSNLELLRISLLIESWLEPVRFLR

SBJCT: 61 YIPKDQKYSFLHDSQTSFCFSDSIPTPSNMEETQOKSNLELLRISLLIESWLEPVRFLR 120

QUERY: 103 SMFANNLVYDTSDDYHLLKDLEEGIQTLMGRLLEDGSRRTGQILKQTYSKFDTNSHNHD 162
SMFANNLVYDTSDDYHLLKDLEEGIQTLMGRLLEDGSRRTGQILKQTYSKFDTNSHNHD

SBJCT: 121 SMFANNLVYDTSDDYHLLKDLEEGIQTLMGRLLEDGSRRTGQILKQTYSKFDTNSHNHD 180

QUERY: 163 ALLKNYGLLYCFRKMDKVETFLRMVQCRSVEGSCGF 199
ALLKNYGLLYCFRKMDKVETFLRMVQCRSVEGSCGF

SBJCT: 181 ALLKNYGLLYCFRKMDKVETFLRMVQCRSVEGSCGF 217

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FIG. 1B

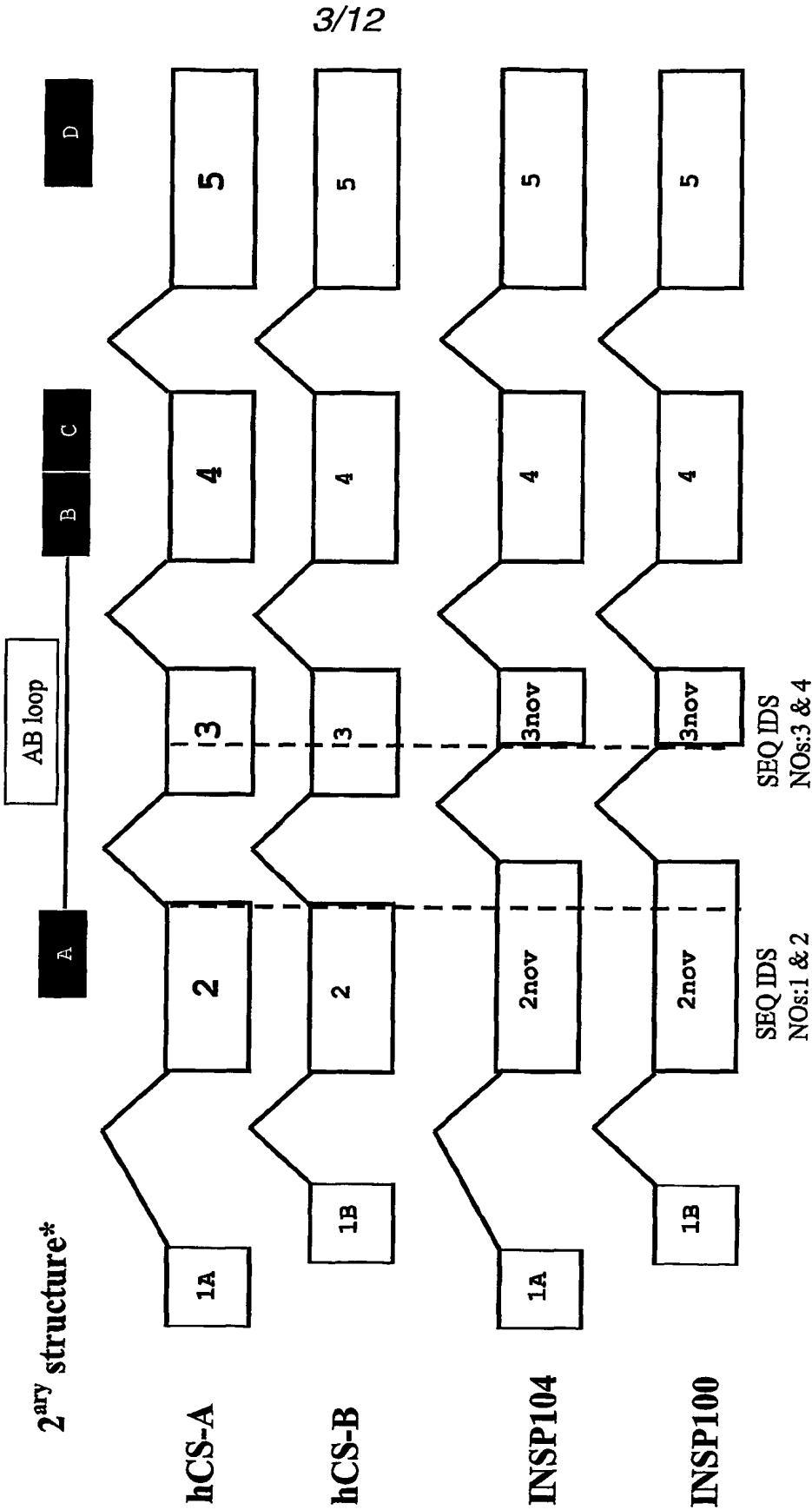
QUERY: 1 MAPGSRTSLLLAFALLCLPWLQEAGAVQTVPLSRLFDHAMLQAHRAHQLAIDTYQEFVSS 60
MAPGSRTSLLLAFALLCLPWLQEAGAVQTVPLSRLFDHAMLQAHRAHQLAIDTYQEF +
SBJCT: 1 MAPGSRTSLLLAFALLCLPWLQEAGAVQTVPLSRLFDHAMLQAHRAHQLAIDTYQEFEEET 60

QUERY: 61 W-----GMSIPTPSNMEETQQKSNLELLRISLLIESWLEPVRFLR 102
+ DSIPTPSNMEETQQKSNLELLRISLLIESWLEPVRFLR
SBJCT: 61 YIPKDQKYSFLHDSQTSFCFSDSIPTPSNMEETQQKSNLELLRISLLIESWLEPVRFLR 120

QUERY: 103 SMFANNLVYDTSDDYHLLKDLEEGIQTLMGRLDGSRRTGQILKQTYSKFDTNSHNHD 162
SMFANNLVYDTSDDYHLLKDLEEGIQTLMGRLDGSRRTGQILKQTYSKFDTNSHNHD
SBJCT: 121 SMFANNLVYDTSDDYHLLKDLEEGIQTLMGRLDGSRRTGQILKQTYSKFDTNSHNHD 180

QUERY: 163 ALLKNYGLLYCFRKMDKVETFLRMVQCRSVEGSCGF 199
ALLKNYGLLYCFRKMDKVETFLRMVQCRSVEGSCGF
SBJCT: 181 ALLKNYGLLYCFRKMDKVETFLRMVQCRSVEGSCGF 217

FIG. 2



*Secondary structure is based on hGH-N structure

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FIG. 3

1 atggctccag gctcccggac gtccctgctc ctggcttttg cctgctctg
m a p g s r t s l l l a f a l l

51 cctgccctgg cttcaagagg ctggtgccgt ccaaaccgtt ccgttatcca
c l p w l q e a g a v q t v p l s

101 ggctttttga ccacgctatg ctccaagccc atcgcgcgca ccagctggcc
r l f d h a m l q a h r a h q l a

151 attgacacct accaggagtt tgtaagttct tggggaatgg actctattcc
i d t y q e f v s s w g m d s i

201 gacaccctcc aacatggagg aaacgcaaca gaaatccaat ctagagctgc
p t p s n m e e t q q k s n l e l

251 tccgcatctc cctgctgctc atcgagtcgt ggctggagcc cgtgcggttc
l r i s l l l i e s w l e p v r f

301 ctcaggagta tggtcgccaa caacctgggtg tatgacacct cggacagcga
l r s m f a n n l v y d t s d s

351 tgactatcac ctctaaagg acctagagga aggcattcaa acgctgatgg
d d y h l l k d l e e g i q t l m

401 ggaggctgga agacggcagc cgccggactg ggcagatcct caagcagacc
g r l e d g s r r t g q i l k q t

451 tacagcaagt ttgacacaaa ctcacacaac catgacgcac tgctcaagaa
y s k f d t n s h n h d a l l k

501 ctacgggctg ctctactgct tcaggaagga catggacaag gtcgagacat
n y g l l y c f r k d m d k v e t

551 tcctgcgcat ggtgcagtgc cgctctgtag agggtagctg tggcttc
f l r m v q c r s v e g s c g f

underlined sequence denotes predicted signal peptide

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FIG. 4

Molecule: product2, 4610 bps DNA Circular

File Name: 13685[1].cm5

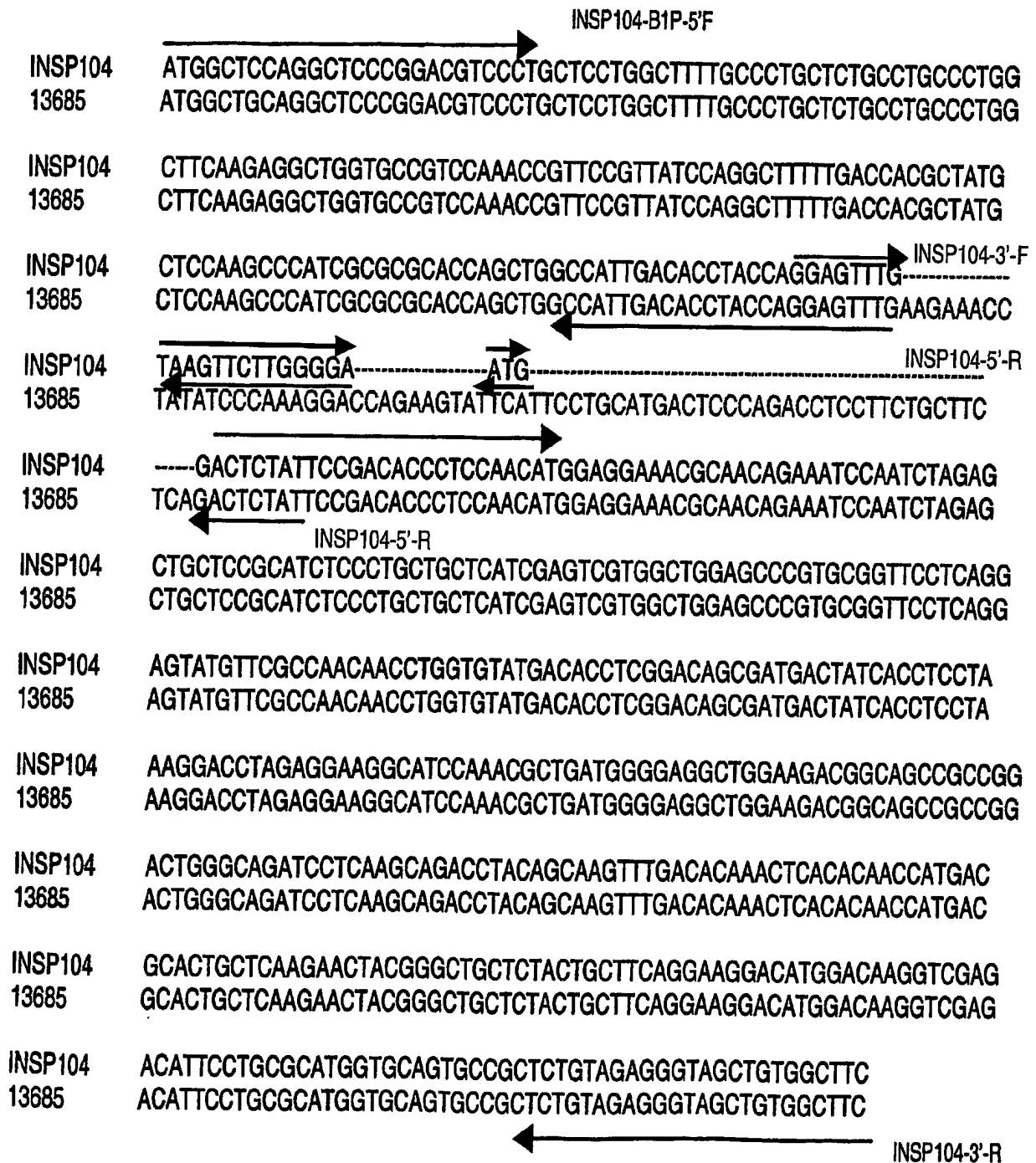
Description: Ligation of inverted NoName into PCRII-TOPO-open

Type	Start	End	Name	Description
GENE	1	336	LacZa'	
REGION	239	256	SP6	Sp6 promoter
GENE	990	340 C	Cds	Inserted cds = BC022044
REGION	996	337 C	Insert	Inserted PCR product
GENE	997	1248	'LacZa	
REGION	1066	1085	T7	T7 promoter
GENE	1250	1664	f1	f1 ori
GENE	1998	2792	KanR	Kanamycin resistance gene
GENE	2810	3670	AmpR	Ampicillin resistance gene
GENE	3815	4488	pUC	pUC ori

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FIG. 5

top = INSP104
bottom = 13685



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FIG. 6

1 acaagtttgt acaaaaaagc aggcttcgcc .accatggctc caggctcccg
m a p g s

51 gacgtccctg ctccctggctt ttgccctgct ctgcctgccc tggcttcaag
r t s l l l a f a l l c l p w l q

101 aggctgggtgc cgtccaaacc gttccgttat ccaggctttt tgaccacgct
e a g a v q t v p l s r l f d h a

151 atgctccaag cccatcgcgc gcaccagctg gccattgaca cctaccagga
m l q a h r a h q l a i d t y q

201 gtttgtaagt tcttggggaa tggactctat tccgacaccc tccaacatgg
e f v s s w g m d s i p t p s n m

251 aggaaacgca acagaaatcc aatctagagc tgctccgcat ctccctgctg
e e t q q k s n l e l l r i s l l

301 ctcacgagct cgtggctgga gcccgtgcgg ttcctcagga gtatgttcgc
l i e s w l e p v r f l r s m f

351 caacaacctg gtgtatgaca cctcggacag cgatgactat cacctcctaa
a n n l v y d t s d s d d y h l l

401 aggacctaga ggaaggcatc caaacgctga tggggaggct ggaagacggc
k d l e e g i q t l m g r l e d g

451 agccgccgga ctgggcagat cctcaagcag acctacagca agtttgacac
s r r t g q i l k q t y s k f d

501 aaactcacac aacctgacg cactgctcaa gaactacggg ctgctctact
t n s h n h d a l l k n y g l l y

551 gcttcaggaa ggacatggac aaggctcaga cattcctgcg catgggtgcag
c f r k d m d k v e t f l r m v q

601 tgccgctctg tagagggtag ctgtggcttc caccatcacc atcaccattg
c r s v e g s c g f h h h h h h

651 aaacccagct ttcttgtaca aagtggg

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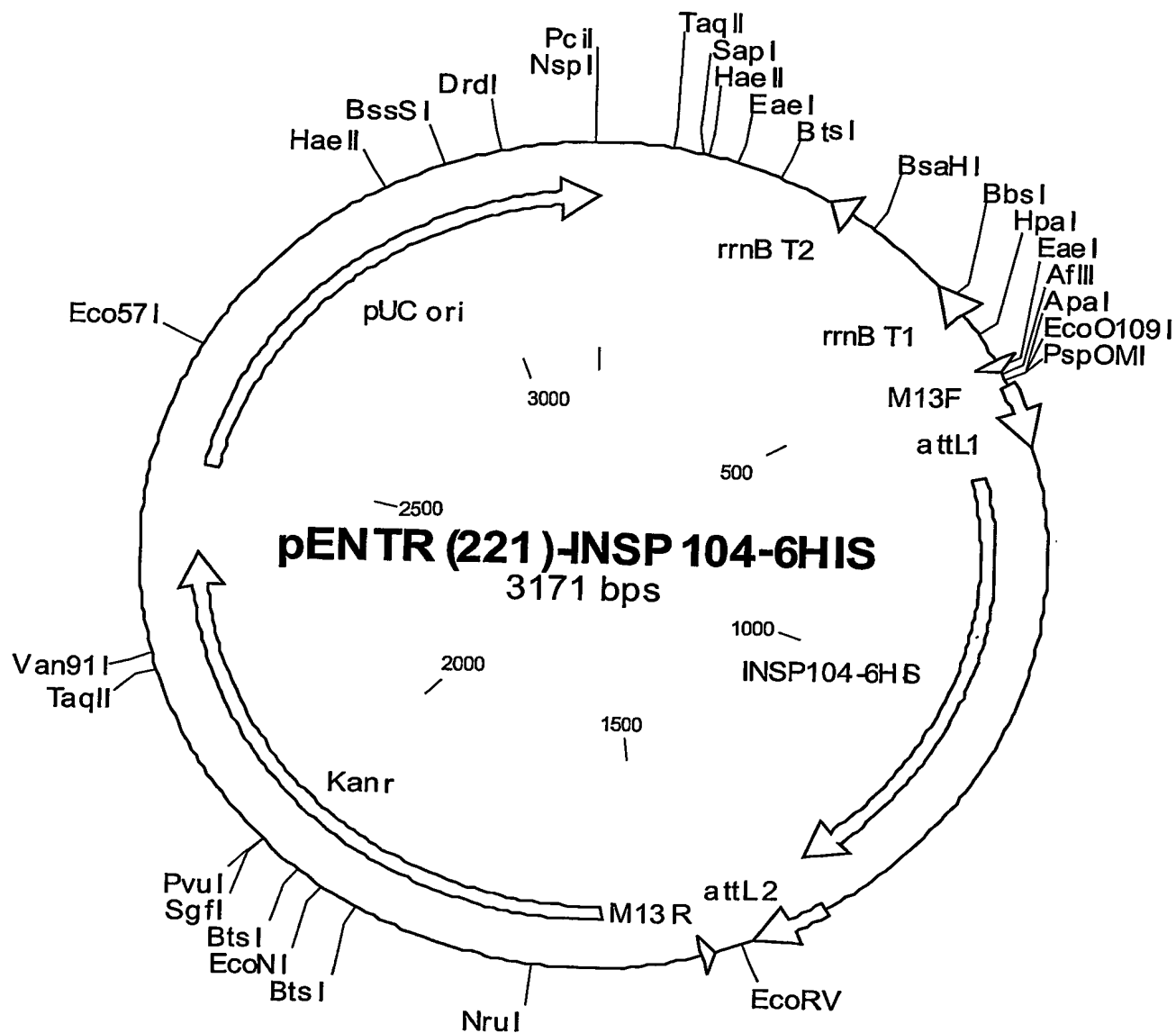
FIG. 7

Molecule: pENTR(221)-INSP104-6HIS, 3171 bps DNA Circular
File Name: pENTR-(DONR221)-INSP104.cm5, dated 20 Nov 2003

Description: Ligation of B1b2-orf.seq* into pDONR221*

Type	Start	End	Name	Description
REGION	295	268	C rrnB T2	transcription termination
sequence				
REGION	470	427	C rrnB T1	transcription termination
sequence				
REGION	537	552	M13F	forward primer
REGION	570	651	attL1	
GENE	677	1291	INSP104-6HIS	
REGION	1306	1394	attL2	
REGION	1452	1436	C M13 R	
GENE	1565	2374	Kan r	
GENE	2495	3168	pUC ori	

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FIG. 7(contd.)

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FIG. 8

Molecule: pEAK12d-INSP104-6HIS-V1, 7564 bps DNA Circular
 File Name: pEAK12d-INSP104-6HIS-V1.cm5, dated 19 Jun 2003

Description: pEAK12 DES with two recombination sites attR1 and attR2
 between which the cDNA is inserted

Type	Start	End	Name	Description
REGION	2	595	pmb-ori	
GENE	596	1519	Amp	
REGION	1690	2795	EF-1alpha	
REGION	2703	2722	peak12-F	forward primer
REGION	2855	2874	attB1	
GENE	2888	3502	INSP104-6HIS	
REGION	3510	3531	attB2	
REGION	3538	3966	'A	poly A/splice
REGION	3652	3633	C peak12-R	reverse primer
GENE	4585	3967	C PUR	PUROMYCIN
REGION	4809	4586	C tK	tK promoter
REGION	5304	4810	C Ori P	
GENE	7356	5304	C EBNA-1	
REGION	7357	7556	sv40	

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FIG. 8(contd.)